



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: KLEIN, Michel H
DU, Run-Pan
EWASYSHYN, Mary E
- (ii) TITLE OF INVENTION: INFECTION DETECTION METHOD USING
CHIMERIC PROTEIN
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sim & McBurney
 - (B) STREET: 6th Floor, 330 University Avenue
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5G 1R7
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/467,961
 - (B) FILING DATE: 06-JUN-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/001,554
 - (B) FILING DATE: 06-JAN-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9200117.1
 - (B) FILING DATE: 06-JAN-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEWART, Michael I
 - (B) REGISTRATION NUMBER: 24,973
 - (C) REFERENCE/DOCKET NUMBER: 1038-1000 MIS:jb
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 595-1155
 - (B) TELEFAX: (416) 595-1163

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1844 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | |
|--|------|
| AAGTCAATAC CAACAACATAT TAGCAGTCAT ACGTGCAAGA ACAAGAAAGA AGAGATTCAA | 60 |
| AAAGCTAAAT AAGAGAAATC AAAACAAAAG GTATAGAACA CCCGAACAAC AAAATCAAAA | 120 |
| CATCCAATCC ATTTTAAACA AAAATTCCAA AAGAGACCGG CAACACAACA AGCACCAAAC | 180 |
| ACAATGCCAA CTTTAATACT GCTAATTATT ACAACAATGA TTATGGCATC TTCCTGCCAA | 240 |
| ATAGATATCA CAAAACTACA GCATGTAGGT GTATTGGTCA ACAGTCCCAA AGGGATGAAG | 300 |
| ATATCACAAA ACTTCGAAAC AAGATATCTA ATTTTGAGCC TCATACCAA AATAGAAGAC | 360 |
| TCTAACTCTT GTGGTGACCA ACAGATCAAA CAATACAAGA GGTATTGGA TAGACTGATC | 420 |
| ATCCCTCTAT ATGATGGATT AAGATTACAG AAAGATGTGA TAGTAACCAA TCAAGAATCC | 480 |
| AATGAAAACA CTGATCCCAG AACAAGACGA TCCTTTGGAG GGGTAATTGG AACCATTGCT | 540 |
| CTGGGAGTAG CAACCTCAGC ACAAATTACA GCGGCAGTTG CTCTGGTTGA AGCCAAGCAG | 600 |
| GCAAAATCAG ACATCGAAAA ACTCAAAGAA GCAATCAGGG ACACAAACAA AGCAGTGCAG | 660 |
| TCAGTTCAGA GCTCTATAGG AAATTTAATA GTAGCAATTA AATCAGTCCA AGATTATGTC | 720 |
| AACAACGAAA TGGTGCCATC GATTGCTAGA CTAGGTTGTG AAGCAGCAGG ACTTCAATTA | 780 |
| GGAATTGCAT TAACACAGCA TTAATCAGAA TTAACAAACA TATTTGGTGA TAACATAGGA | 840 |
| TCGTTACAAG AAAAAGGAAT AAAATTACAA GGTATAGCAT CATTATACCG CACAAATATC | 900 |
| ACAGAAATAT TCACAACATC AACAGTTGAT AAATATGATA TCTATGATCT ATTATTTACA | 960 |
| GAATCAATAA AGGTGAGAGT TATAGATGTT GATTTGAATG ATTACTCAAT CACCCTCCAA | 1020 |
| GTCAGACTCC CTTTATTAAC TAGGCTGCTG AACACTCAGA TCTACAAAGT AGATTCCATA | 1080 |
| TCATATAATA TCCAAAACAG AGAATGGTAT ATCCCTCTTC CCAGCCATAT CATGACGAAA | 1140 |
| GGGGCATTTC TAGGTGGAGC AGATGTCAAG GAATGTATAG AAGCATTGAG CAGTTATATA | 1200 |
| TGCCCTTCTG ATCCAGGATT TGTACTAAAC CATGAAATGG AGAGCTGCTT ATCAGGAAAC | 1260 |
| ATATCCCAAT GTCCAAGAAC CACGGTCACA TCAGACATTG TTCCAAGATA TGCATTTGTC | 1320 |
| AATGGAGGAG TGGTTGCAAA CTGTATAACA ACCACCTGTA CATGCAACGG AATCGACAAT | 1380 |

| | |
|---|------|
| AGAATCAATC AACCACCTGA TCAAGGAGTA AAAATTATAA CACATAAAGA ATGTAATACA | 1440 |
| ATAGGTATCA ACGGAATGCT GTTCAATACA AATAAAGAAG GAACTCTTGC ATTCTACACA | 1500 |
| CCAAATGATA TAACACTAAA TAATTCTGTT GCACTTGATC CAATTGACAT ATCAATCGAG | 1560 |
| CTTAACAAAG CCAAATCAGA TCTAGAAGAA TCAAAAGAAT GGATAAGAAG GTCAAATCAA | 1620 |
| AAACTAGATT CTATTGAAA CTGGCATCAA TCTAGCACTA CAATCATAAT TATTTTAATA | 1680 |
| ATGATCATT TATTGTTTAT AATTAATGTA ACGATAATTA CAATTGCAAT TAAGTATTAC | 1740 |
| AGAATTCAAA AGAGAAATCG AGTGGATCAA AATGACAAGC CATATGTACT AACAAACAAA | 1800 |
| TGACATATCT ATAGATCATT AGATATTAAA ATTATAAAAA ACTT | 1844 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Thr | Leu | Ile | Leu | Leu | Ile | Ile | Thr | Thr | Met | Ile | Met | Ala | Ser |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Ser | Cys | Gln | Ile | Asp | Ile | Thr | Lys | Leu | Gln | His | Val | Gly | Val | Leu | Val |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| Asn | Ser | Pro | Lys | Gly | Met | Lys | Ile | Ser | Gln | Asn | Phe | Glu | Thr | Arg | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Ile | Leu | Ser | Leu | Ile | Pro | Lys | Ile | Glu | Asp | Ser | Asn | Ser | Cys | Gly |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Asp | Gln | Gln | Ile | Lys | Gln | Tyr | Lys | Arg | Leu | Leu | Asp | Arg | Leu | Ile | Ile |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Pro | Leu | Tyr | Asp | Gly | Leu | Arg | Leu | Gln | Lys | Asp | Val | Ile | Val | Thr | Asn |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Gln | Glu | Ser | Asn | Glu | Asn | Thr | Asp | Pro | Arg | Thr | Arg | Arg | Ser | Phe | Gly |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Val | Ile | Gly | Thr | Ile | Ala | Leu | Gly | Val | Ala | Thr | Ser | Ala | Gln | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Thr | Ala | Ala | Val | Ala | Leu | Val | Glu | Ala | Lys | Gln | Ala | Lys | Ser | Asp | Ile |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Glu | Lys | Leu | Lys | Glu | Ala | Ile | Arg | Asp | Thr | Asn | Lys | Ala | Val | Gln | Ser |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | | 150 | | 155 | | 160 | | | | | | | | | |
| Val | Gln | Ser | Ser | Ile | Gly | Asn | Leu | Ile | Val | Ala | Ile | Lys | Ser | Val | Gln |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asp | Tyr | Val | Asn | Asn | Glu | Ile | Val | Pro | Ser | Ile | Ala | Arg | Leu | Gly | Cys |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Glu | Ala | Ala | Gly | Leu | Gln | Leu | Gly | Ile | Ala | Leu | Thr | Gln | His | Tyr | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Glu | Leu | Thr | Asn | Ile | Phe | Gly | Asp | Asn | Ile | Gly | Ser | Leu | Gln | Glu | Lys |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Gly | Ile | Lys | Leu | Gln | Gly | Ile | Ala | Ser | Leu | Tyr | Arg | Thr | Asn | Ile | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Glu | Ile | Phe | Thr | Thr | Ser | Thr | Val | Asp | Lys | Tyr | Asp | Ile | Tyr | Asp | Leu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Phe | Thr | Glu | Ser | Ile | Lys | Val | Arg | Val | Ile | Asp | Val | Asp | Leu | Asn |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asp | Tyr | Ser | Ile | Thr | Leu | Gln | Val | Arg | Leu | Pro | Leu | Leu | Thr | Arg | Leu |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Leu | Asn | Thr | Gln | Ile | Tyr | Lys | Val | Asp | Ser | Ile | Ser | Tyr | Asn | Ile | Gln |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asn | Arg | Glu | Trp | Tyr | Ile | Pro | Leu | Pro | Ser | His | Ile | Met | Thr | Lys | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ala | Phe | Leu | Gly | Gly | Ala | Asp | Val | Lys | Glu | Cys | Ile | Glu | Ala | Phe | Ser |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Ser | Tyr | Ile | Cys | Pro | Ser | Asp | Pro | Gly | Phe | Val | Leu | Asn | His | Glu | Met |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Glu | Ser | Cys | Leu | Ser | Gly | Asn | Ile | Ser | Gln | Cys | Pro | Arg | Thr | Thr | Val |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Thr | Ser | Asp | Ile | Val | Pro | Arg | Tyr | Ala | Phe | Val | Asn | Gly | Gly | Val | Val |
| | | 370 | | | | 375 | | | | | 380 | | | | |
| Ala | Asn | Cys | Ile | Thr | Thr | Thr | Cys | Thr | Cys | Asn | Gly | Ile | Asp | Asn | Arg |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ile | Asn | Gln | Pro | Pro | Asp | Gln | Gly | Val | Lys | Ile | Ile | Thr | His | Lys | Glu |
| | | | 405 | | | | | | 410 | | | | | 415 | |
| Cys | Asn | Thr | Ile | Gly | Ile | Asn | Gly | Met | Leu | Phe | Asn | Thr | Asn | Lys | Glu |
| | | | 420 | | | | 425 | | | | | | 430 | | |
| Gly | Thr | Leu | Ala | Phe | Tyr | Thr | Pro | Asn | Asp | Ile | Thr | Leu | Asn | Asn | Ser |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Val | Ala | Leu | Asp | Pro | Ile | Asp | Ile | Ser | Ile | Glu | Leu | Asn | Lys | Ala | Lys |

| | | |
|---|-----|---------|
| 450 | 455 | 460 |
| Ser Asp Leu Glu Glu Ser Lys Glu Trp Ile Arg Arg Ser Asn Gln Lys | | |
| 465 | 470 | 475 480 |
| Leu Asp Ser Ile Gly Asn Trp His Gln Ser Ser Thr Thr Ile Ile Ile | | |
| | 485 | 490 495 |
| Ile Leu Ile Met Ile Ile Ile Leu Phe Ile Ile Asn Val Thr Ile Ile | | |
| | 500 | 505 510 |
| Thr Ile Ala Ile Lys Tyr Tyr Arg Ile Gln Lys Arg Asn Arg Val Asp | | |
| | 515 | 520 525 |
| Gln Asn Asp Lys Pro Tyr Val Leu Thr Asn Lys | | |
| | 530 | 535 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1833 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | |
|---|-----|
| AGACAAATCC AAATTCGAGA TGGAATACTG GAAGCATACC AATCACGGAA AGGATGCTGG | 60 |
| CAATGAGCTG GAGACGTCCA TGGCTACTAA TGGCAACAAG CTCACCAATA AGATAACATA | 120 |
| TATATTATGG ACAATAATCC TGGTGTATT ATCAATAGTC TTCATCATAG TGCTAATTAA | 180 |
| TTCCATCAAA AGTGAAAAGG CTCATGAATC ATTGCTGCAA GACATAAATA ATGAGTTTAT | 240 |
| GGAAATTACA GAAAAGATCC AAATGGCATC GGATAATACC AATGATCTAA TACAGTCAGG | 300 |
| AGTGAATACA AGGCTTCTTA CAATTCAGAG TCATGTCCAG AATTATATAC CAATATCACT | 360 |
| GACACAACAG ATGTCAGATC TTAGGAAATT CATTAGTGAA ATTACAATTA GAAATGATAA | 420 |
| TCAAGAAGTG CTGCCACAAA GAATAACACA TGATGTGGGT ATAAAACCTT TAAATCCAGA | 480 |
| TGATTTTTGG AGATGCACGT CTGGTCTTCC ATCTTTAATG AAAACTCCAA AAATAAGGTT | 540 |
| AATGCCAGGG CCGGGATTAT TAGCTATGCC AACGACTGTT GATGGCTGTA TCAGAACTCC | 600 |
| GTCCTTAGTT ATAAATGATC TGATTTATGC TTATACCTCA AATCTAATTA CTCGAGGTTG | 660 |
| TCAGGATATA GGAAATCAT ATCAAGTCTT ACAGATAGGG ATAATAACTG TAAACTCAGA | 720 |
| CTTGGTACCT GACTTAAATC CCAGGATCTC TCATACTTTT AACATAAATG ACAATAGGAA | 780 |
| GTCATGTTCT CTAGCACTCC TAAATACAGA TGTATATCAA CTGTGTTCAA CTCCCAAAGT | 840 |

| | |
|---|------|
| TGATGAAAGA TCAGATTATG CATCATCAGG CATAGAAGAT ATTGTACTTG ATATTGTCAA | 900 |
| TTATGATGGC TCAATCTCAA CAACAAGATT TAAGAATAAT AACATAAGCT TTGATCAACC | 960 |
| TTATGCTGCA CTATACCCAT CTGTTGGACC AGGGATATAC TACAAAGGCA AAATAATATT | 1020 |
| TCTCGGGTAT GGAGGTCCTG AACATCCAAT AAATGAGAAT GTAATCTGCA ACACAACTGG | 1080 |
| GTGTCCCGGG AAAACACAGA GAGACTGCAA TCAGGCATCT CATAGTCCAT GGTTTTCAGA | 1140 |
| TAGGAGGATG GTCAACTCTA TCATTGTTGT TGACAAAGGC TTAAACTCAA TTCCAAAATT | 1200 |
| GAAGGTATGG ACGATATCTA TGAGACAGAA TTACTGGGGG TCAGAAGGAA GGTTACTTCT | 1260 |
| ACTAGGTAAC AAGATCTATA TATATACAAG ATCCACAAGT TGGCATAGCA AGTTACAATT | 1320 |
| AGGAATAATT GATATTACTG ATTACAGTGA TATAAGGATA AAATGGACAT GGCATAATGT | 1380 |
| GCTATCAAGA CCAGGAAACA ATGAATGTCC ATGGGGACAT TCATGTCCAG ATGGATGTAT | 1440 |
| AACAGGAGTA TATACTGATG CATATCCACT CAATCCCACA GGGAGCATTG TGTCACTGT | 1500 |
| CATATTAGAT TCACAAAAAT CGAGAGTGAA CCCAGTCATA ACTTACTCAA CAGCAACCGA | 1560 |
| AAGAGTAAAC GAGCTGGCCA TCCGAAACAG AACACTCTCA GCTGGATATA CAACAACAAG | 1620 |
| CTGCATCACA CACTATAACA AAGGATATTG TTTTCATATA GTAGAAATAA ATCAGAAAAG | 1680 |
| CTTAAACACA CTTCAACCCA TGTTGTTCAA GACAGAGGTT CCAAAAAGCT GCAGTTAATC | 1740 |
| ATAATTAACC GCAATATGCA TTAACCTATC TATAATACAA GTATATGATA AGTAATCAGC | 1800 |
| AATCAGACAA TAGACAAAAG GGAAATATAA AAA | 1833 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Tyr | Trp | Lys | His | Thr | Asn | His | Gly | Lys | Asp | Ala | Gly | Asn | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Glu | Thr | Ser | Met | Ala | Thr | Asn | Gly | Asn | Lys | Leu | Thr | Asn | Lys | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Tyr | Ile | Leu | Trp | Thr | Ile | Ile | Leu | Val | Leu | Leu | Ser | Ile | Val | Phe |
| | | | 35 | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Ile | Val | Leu | Ile | Asn | Ser | Ile | Lys | Ser | Glu | Lys | Ala | His | Glu | Ser | |
| 50 | | | | | | 55 | | | | | 60 | | | | | |
| Leu | Leu | Gln | Asp | Ile | Asn | Asn | Glu | Phe | Met | Glu | Ile | Thr | Glu | Lys | Ile | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Gln | Met | Ala | Ser | Asp | Asn | Thr | Asn | Asp | Leu | Ile | Gln | Ser | Gly | Val | Asn | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Thr | Arg | Leu | Leu | Thr | Ile | Gln | Ser | His | Val | Gln | Asn | Tyr | Ile | Pro | Ile | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ser | Leu | Thr | Gln | Gln | Met | Ser | Asp | Leu | Arg | Lys | Phe | Ile | Ser | Glu | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Thr | Ile | Arg | Asn | Asp | Asn | Gln | Glu | Val | Leu | Pro | Gln | Arg | Ile | Thr | His | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Asp | Val | Gly | Ile | Lys | Pro | Leu | Asn | Pro | Asp | Asp | Phe | Trp | Arg | Cys | Thr | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | |
| Ser | Gly | Leu | Pro | Ser | Leu | Met | Lys | Thr | Pro | Lys | Ile | Arg | Leu | Met | Pro | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Gly | Pro | Gly | Leu | Leu | Ala | Met | Pro | Thr | Thr | Val | Asp | Gly | Cys | Ile | Arg | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Thr | Pro | Ser | Leu | Val | Ile | Asn | Asp | Leu | Ile | Tyr | Ala | Tyr | Thr | Ser | Asn | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Leu | Ile | Thr | Arg | Gly | Cys | Gln | Asp | Ile | Gly | Lys | Ser | Tyr | Gln | Val | Leu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Gln | Ile | Gly | Ile | Ile | Thr | Val | Asn | Ser | Asp | Leu | Val | Pro | Asp | Leu | Asn | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Pro | Arg | Ile | Ser | His | Thr | Phe | Asn | Ile | Asn | Asp | Asn | Arg | Lys | Ser | Cys | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ser | Leu | Ala | Leu | Leu | Asn | Thr | Asp | Val | Tyr | Gln | Leu | Cys | Ser | Thr | Pro | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Lys | Val | Asp | Glu | Arg | Ser | Asp | Tyr | Ala | Ser | Ser | Gly | Ile | Glu | Asp | Ile | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Val | Leu | Asp | Ile | Val | Asn | Tyr | Asp | Gly | Ser | Ile | Ser | Thr | Thr | Arg | Phe | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Lys | Asn | Asn | Asn | Ile | Ser | Phe | Asp | Gln | Pro | Tyr | Ala | Ala | Leu | Tyr | Pro | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Ser | Val | Gly | Pro | Gly | Ile | Tyr | Tyr | Lys | Gly | Lys | Ile | Ile | Phe | Leu | Gly | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Tyr | Gly | Gly | Leu | Glu | His | Pro | Ile | Asn | Glu | Asn | Val | Ile | Cys | Asn | Thr | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Gly | Cys | Pro | Gly | Lys | Thr | Gln | Arg | Asp | Cys | Asn | Gln | Ala | Ser | His | 355 | 360 | 365 | |
| Ser | Pro | Trp | Phe | Ser | Asp | Arg | Arg | Met | Val | Asn | Ser | Ile | Ile | Val | Val | 370 | 375 | 380 | |
| Asp | Lys | Gly | Leu | Asn | Ser | Ile | Pro | Lys | Leu | Lys | Val | Trp | Thr | Ile | Ser | 385 | 390 | 395 | 400 |
| Met | Arg | Gln | Asn | Tyr | Trp | Gly | Ser | Glu | Gly | Arg | Leu | Leu | Leu | Leu | Gly | 405 | 410 | 415 | |
| Asn | Lys | Ile | Tyr | Ile | Tyr | Thr | Arg | Ser | Thr | Ser | Trp | His | Ser | Lys | Leu | 420 | 425 | 430 | |
| Gln | Leu | Gly | Ile | Ile | Asp | Ile | Thr | Asp | Tyr | Ser | Asp | Ile | Arg | Ile | Lys | 435 | 440 | 445 | |
| Trp | Thr | Trp | His | Asn | Val | Leu | Ser | Arg | Pro | Gly | Asn | Asn | Glu | Cys | Pro | 450 | 455 | 460 | |
| Trp | Gly | His | Ser | Cys | Pro | Asp | Gly | Cys | Ile | Thr | Gly | Val | Tyr | Thr | Asp | 465 | 470 | 475 | 480 |
| Ala | Tyr | Pro | Leu | Asn | Pro | Thr | Gly | Ser | Ile | Val | Ser | Ser | Val | Ile | Leu | 485 | 490 | 495 | |
| Asp | Ser | Gln | Lys | Ser | Arg | Val | Asn | Pro | Val | Ile | Thr | Tyr | Ser | Thr | Ala | 500 | 505 | 510 | |
| Thr | Glu | Arg | Val | Asn | Glu | Leu | Ala | Ile | Arg | Asn | Arg | Thr | Leu | Ser | Ala | 515 | 520 | 525 | |
| Gly | Tyr | Thr | Thr | Thr | Ser | Cys | Ile | Thr | His | Tyr | Asn | Lys | Gly | Tyr | Cys | 530 | 535 | 540 | |
| Phe | His | Ile | Val | Glu | Ile | Asn | Gln | Lys | Ser | Leu | Asn | Thr | Leu | Gln | Pro | 545 | 550 | 555 | 560 |
| Met | Leu | Phe | Lys | Thr | Glu | Val | Pro | Lys | Ser | Cys | Ser | | | | | 565 | 570 | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1886 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGAGTTGC CAATCCTCAA AGCAAATGCA ATTACCACAA TCCTCGCTGC AGTCACATTT

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|------|
| TGCTTTGCTT | CTAGTCAAAA | CATCACTGAA | GAATTTTATC | AATCAACATG | CAGTGCAGTT | 120 |
| AGCAAAGGCT | ATCTTAGTGC | TCTAAGAACT | GGTTGGTATA | CTAGTGTAT | AACTATAGAA | 180 |
| TTAAGTAATA | TCAAGGAAAA | TAAGTGTAAT | GGAACAGATG | CTAAGGTAAA | ATTGATGAAA | 240 |
| CAAGAATTAG | ATAAATATAA | AAATGCTGTA | ACAGAATTGC | AGTTGCTCAT | GCAAAGCACA | 300 |
| CCAGCAGCAA | ACAATCGAGC | CAGAAGAGAA | CTACCAAGGT | TTATGAATTA | TACACTCAAC | 360 |
| AATACCAAAA | AAACCAATGT | AACATTAAGC | AAGAAAAGGA | AAAGAAGATT | TCTTGGTTTT | 420 |
| TTGTTAGGTG | TTGGATCTGC | AATCGCCAGT | GGCATTGCTG | TATCTAAGGT | CCTGCACTTA | 480 |
| GAAGGAGAAG | TGAACAAGAT | CAAAAGTGCT | CTACTATCCA | CAAACAAGGC | CGTAGTCAGC | 540 |
| TTATCAAATG | GAGTTAGTGT | CTTAACCAGC | AAAGTGTTAG | ACCTCAAAAA | CTATATAGAT | 600 |
| AAACAATTGT | TACCTATTGT | GAATAAGCAA | AGCTGCAGAA | TATCAAATAT | AGAAACTGTG | 660 |
| ATAGAGTTCC | AACAAAAGAA | CAACAGACTA | CTAGAGATTA | CCAGGGAATT | TAGTGTTAAT | 720 |
| GCAGGTGTAA | CTACACCTGT | AAGCACTTAC | ATGTTAACTA | ATAGTGAATT | ATTGTCATTA | 780 |
| ATCAATGATA | TGCCATAAAC | AAATGATCAG | AAAAAGTTAA | TGTCCAACAA | TGTTCAAATA | 840 |
| GTTAGACAGC | AAAGTTACTC | TATCATGTCC | ATAATAAAAG | AGGAAGTCTT | AGCATATGTA | 900 |
| GTACAATTAC | CACTATATGG | TGTGATAGAT | ACACCTTGTT | GGAAATTACA | CACATCCCCCT | 960 |
| CTATGTACAA | CCAACACAAA | AGAAGGGTCA | AACATCTGTT | TAACAAGAAC | TGACAGAGGA | 1020 |
| TGGTACTGTG | ACAATGCAGG | ATCAGTATCT | TTCTTCCCAC | AAGCTGAAAC | ATGTAAAGTT | 1080 |
| CAATCGAATC | GAGTATTTTG | TGACACAATG | AACAGTTTAA | CATTACCAAG | TGAAGTAAAT | 1140 |
| CTCTGCAATG | TTGACATATT | CAATCCCAAA | TATGATTGTA | AAATTATGAC | TTCAAAAACA | 1200 |
| GATGTAAGCA | GCTCCGTTAT | CACATCTCTA | GGAGCCATTG | TGTCATGCTA | TGGCAAAACT | 1260 |
| AAATGTACAG | CATCCAATAA | AAATCGTGGA | ATCATAAAGA | CATTTTCTAA | CGGGTGTGAT | 1320 |
| TATGTATCAA | ATAAAGGGGT | GGACACTGTG | TCTGTAGGTA | ACACATTATA | TTATGTAAAT | 1380 |
| AAGCAAGAAG | GCAAAAGTCT | CTATGTAAAA | GGTGAACCAA | TAATAAATTT | CTATGACCCA | 1440 |
| TTAGTATTCC | CCTCTGATGA | ATTTGATGCA | TCAATATCTC | AAGTCAATGA | GAAGATTAAC | 1500 |
| CAGAGTTTAG | CATTTATTCTG | TAAATCCGAT | GAATTATTAC | ATAATGTAAA | TGCTGGTAAA | 1560 |
| TCAACCACAA | ATATCATGAT | AACTACTATA | ATTATAGTGA | TTATAGTAAT | ATTGTTATCA | 1620 |
| TTAATTGCTG | TTGGACTGCT | CCTATACTGT | AAGGCCAGAA | GCACACCAGT | CACACTAAGC | 1680 |
| AAGGATCAAC | TGAGTGGTAT | AAATAATATT | GCATTTAGTA | ACTGAATAAA | AATAGCACCT | 1740 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AATCATGTTT | TTACAATGGT | TTACTATCTG | CTCATAGACA | ACCCATCTAT | CATTGGATTT | 1800 |
| TCTTAAAATC | TGAACTTCAT | CGAAACTCTT | ATCTATAAAC | CATCTCACTT | ACACTATTTA | 1860 |
| AGTAGATTCC | TAGTTTATAG | TTATAT | | | | 1886 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Pro | Ile | Leu | Lys | Ala | Asn | Ala | Ile | Thr | Thr | Ile | Leu | Ala | 1 | 5 | 10 | 15 |
| Ala | Val | Thr | Phe | Cys | Phe | Ala | Ser | Ser | Gln | Asn | Ile | Thr | Glu | Glu | Phe | 20 | 25 | 30 | |
| Tyr | Gln | Ser | Thr | Cys | Ser | Ala | Val | Ser | Lys | Gly | Tyr | Leu | Ser | Ala | Leu | 35 | 40 | 45 | |
| Arg | Thr | Gly | Trp | Tyr | Thr | Ser | Val | Ile | Thr | Ile | Glu | Leu | Ser | Asn | Ile | 50 | 55 | 60 | |
| Lys | Glu | Asn | Lys | Cys | Asn | Gly | Thr | Asp | Ala | Lys | Val | Lys | Leu | Met | Lys | 65 | 70 | 75 | 80 |
| Gln | Glu | Leu | Asp | Lys | Tyr | Lys | Asn | Ala | Val | Thr | Glu | Leu | Gln | Leu | Leu | 85 | 90 | 95 | |
| Met | Gln | Ser | Thr | Pro | Ala | Ala | Asn | Asn | Arg | Ala | Arg | Arg | Glu | Leu | Pro | 100 | 105 | 110 | |
| Arg | Phe | Met | Asn | Tyr | Thr | Leu | Asn | Asn | Thr | Lys | Lys | Thr | Asn | Val | Thr | 115 | 120 | 125 | |
| Leu | Ser | Lys | Lys | Arg | Lys | Arg | Arg | Phe | Leu | Gly | Phe | Leu | Leu | Gly | Val | 130 | 135 | 140 | |
| Gly | Ser | Ala | Ile | Ala | Ser | Gly | Ile | Ala | Val | Ser | Lys | Val | Leu | His | Leu | 145 | 150 | 155 | 160 |
| Glu | Gly | Glu | Val | Asn | Lys | Ile | Lys | Ser | Ala | Leu | Leu | Ser | Thr | Asn | Lys | 165 | 170 | 175 | |
| Ala | Val | Val | Ser | Leu | Ser | Asn | Gly | Val | Ser | Val | Leu | Thr | Ser | Lys | Val | 180 | 185 | 190 | |
| Leu | Asp | Leu | Lys | Asn | Tyr | Ile | Asp | Lys | Gln | Leu | Leu | Pro | Ile | Val | Asn | 195 | 200 | 205 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Gln | Ser | Cys | Arg | Ile | Ser | Asn | Ile | Glu | Thr | Val | Ile | Glu | Phe | Gln | 210 | 215 | 220 | |
| His | Lys | Asn | Asn | Arg | Leu | Leu | Glu | Ile | Thr | Arg | Glu | Phe | Ser | Val | Asn | 225 | 230 | 235 | 240 |
| Ala | Gly | Val | Thr | Thr | Pro | Val | Ser | Thr | Tyr | Met | Leu | Thr | Asn | Ser | Glu | 245 | 250 | 255 | |
| Leu | Leu | Ser | Leu | Ile | Asn | Asp | Met | Pro | Ile | Thr | Asn | Asp | Gln | Lys | Lys | 260 | 265 | 270 | |
| Leu | Met | Ser | Asn | Asn | Val | Gln | Ile | Val | Arg | Gln | Gln | Ser | Tyr | Ser | Ile | 275 | 280 | 285 | |
| Met | Ser | Ile | Ile | Lys | Glu | Glu | Val | Leu | Ala | Tyr | Val | Val | Gln | Leu | Pro | 290 | 295 | 300 | |
| Leu | Tyr | Gly | Val | Ile | Asp | Thr | Pro | Cys | Trp | Lys | Leu | His | Thr | Ser | Pro | 305 | 310 | 315 | 320 |
| Leu | Cys | Thr | Thr | Asn | Thr | Lys | Glu | Gly | Ser | Asn | Ile | Cys | Leu | Thr | Arg | 325 | 330 | 335 | |
| Thr | Asp | Arg | Gly | Trp | Tyr | Cys | Asp | Asn | Ala | Gly | Ser | Val | Ser | Phe | Phe | 340 | 345 | 350 | |
| Pro | Gln | Ala | Glu | Thr | Cys | Lys | Val | Gln | Ser | Asn | Arg | Val | Phe | Cys | Asp | 355 | 360 | 365 | |
| Thr | Met | Asn | Ser | Leu | Thr | Leu | Pro | Ser | Glu | Val | Asn | Leu | Cys | Asn | Val | 370 | 375 | 380 | |
| Asp | Ile | Phe | Asn | Pro | Lys | Tyr | Asp | Cys | Lys | Ile | Met | Thr | Ser | Lys | Thr | 385 | 390 | 395 | 400 |
| Asp | Val | Ser | Ser | Ser | Val | Ile | Thr | Ser | Leu | Gly | Ala | Ile | Val | Ser | Cys | 405 | 410 | 415 | |
| Tyr | Gly | Lys | Thr | Lys | Cys | Thr | Ala | Ser | Asn | Lys | Asn | Arg | Gly | Ile | Ile | 420 | 425 | 430 | |
| Lys | Thr | Phe | Ser | Asn | Gly | Cys | Asp | Tyr | Val | Ser | Asn | Lys | Gly | Val | Asp | 435 | 440 | 445 | |
| Thr | Val | Ser | Val | Gly | Asn | Thr | Leu | Tyr | Tyr | Val | Asn | Lys | Gln | Glu | Gly | 450 | 455 | 460 | |
| Lys | Ser | Leu | Tyr | Val | Lys | Gly | Glu | Pro | Ile | Ile | Asn | Phe | Tyr | Asp | Pro | 465 | 470 | 475 | 480 |
| Leu | Val | Phe | Pro | Ser | Asp | Glu | Phe | Asp | Ala | Ser | Ile | Ser | Gln | Val | Asn | 485 | 490 | 495 | |
| Glu | Lys | Ile | Asn | Leu | Val | Phe | Pro | Ser | Asp | Glu | Phe | Asp | Ala | Ser | Ile | 500 | 505 | 510 | |

Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys
 515 520 525
 Ser Asp Glu Leu Leu His Asn Val Asn Ala Gly Lys Ser Thr Thr Asn
 530 535 540
 Ile Met Ile Thr Thr Ile Ile Ile Glu Ile Ile Val Ile Leu Leu Ser
 545 550 555 560
 Leu Ile Ala Val Gly Leu Leu Leu Tyr Cys Lys Ala Arg Ser Thr Pro
 565 570 575
 Val Thr Leu Ser Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe
 580 585 590
 Ser Asn

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 920 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | |
|---|-----|
| TGCAAACATG TCCAAAAACA AGGACCAACG CACCGCTAAG AACTAGAAA AGACCTGGGA | 60 |
| CACTCTCAAT CATTTATTAT TCATATCATC GGGCTTATAT AAGTTAAATC TTAAATCTGT | 120 |
| AGCACAAATC ACATTATCCA TTCTGGCAAT GATAATCTCA ACTTCACTTA TAATTACAGC | 180 |
| CATCATATTC ATAGCCTCGG CAAACCACAA AGTCACACTA ACAACTGCAA TCATACAAGA | 240 |
| TGCAACAAGC CAGATCAAGA ACACAACCCC AACATACCTC ACTCAGGATC CTCAGCTTGG | 300 |
| AATCAGCTTC TCCAATCTGT CTGAAATTAC ATCACAAACC ACCACCATAC TAGCTTCAAC | 360 |
| AACACCAGGA GTCAAGTCAA ACCTGCAACC CACAACAGTC AAGACTAAAA ACACAACAAC | 420 |
| AACCCAAACA CAACCCAGCA AGCCCACTAC AAAACAACGC CAAAACAAAC CACCAAACAA | 480 |
| ACCCAATAAT GATTTTCACT TCGAAGTGTT TAACTTTGTA CCCTGCAGCA TATGCAGCAA | 540 |
| CAATCCAACC TGCTGGGCTA TCTGCAAAAG AATACCAAAC AAAAAACCAG GAAAGAAAAC | 600 |
| CACCACCAAG CCTACAAAAA AACCAACCTT CAAGACAACC AAAAAAGATC TCAAACCTCA | 660 |
| AACCACTAAA CCAAAGGAAG TACCCACCAC CAAGCCCACA GAAGAGCCAA CCATCAACAC | 720 |

| | |
|---|-----|
| CACCAAAACA AACATCACAA CTACACTGCT CACCAACAAC ACCACAGGAA ATCCAAAAC | 780 |
| CACAAGTCAA ATGGAAACCT TCCACTCAAC CTCCTCCGAA GGCAATCTAA GCCCTTCTCA | 840 |
| AGTCTCCACA ACATCCGAGC ACCCATCACA ACCCTCATCT CCACCCAACA CAACACGCCA | 900 |
| GTAGTTATTA AAAAAAAAAA | 920 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Asn | Lys | Asp | Gln | Arg | Thr | Ala | Lys | Thr | Leu | Glu | Lys | Thr | 1 | 5 | 10 | 15 |
| Trp | Asp | Thr | Leu | Asn | His | Leu | Leu | Phe | Ile | Ser | Ser | Gly | Leu | Tyr | Lys | 20 | 25 | 30 | |
| Leu | Asn | Leu | Lys | Ser | Val | Ala | Gln | Ile | Thr | Leu | Ser | Ile | Leu | Ala | Met | 35 | 40 | 45 | |
| Ile | Ile | Ser | Thr | Ser | Leu | Ile | Ile | Thr | Ala | Ile | Ile | Phe | Ile | Ala | Ser | 50 | 55 | 60 | |
| Ala | Asn | His | Lys | Val | Thr | Leu | Thr | Thr | Ala | Ile | Ile | Gln | Asp | Ala | Thr | 65 | 70 | 75 | 80 |
| Ser | Gln | Ile | Lys | Asn | Thr | Thr | Pro | Thr | Tyr | Leu | Thr | Gln | Asp | Pro | Gln | 85 | 90 | 95 | |
| Leu | Gly | Ile | Ser | Phe | Ser | Asn | Leu | Ser | Glu | Ile | Thr | Ser | Gln | Thr | Thr | 100 | 105 | 110 | |
| Thr | Ile | Leu | Ala | Ser | Thr | Thr | Pro | Gly | Val | Lys | Ser | Asn | Leu | Gln | Pro | 115 | 120 | 125 | |
| Thr | Thr | Val | Lys | Thr | Lys | Asn | Thr | Thr | Thr | Thr | Gln | Thr | Gln | Pro | Ser | 130 | 135 | 140 | |
| Lys | Pro | Thr | Thr | Lys | Gln | Arg | Gln | Asn | Lys | Pro | Pro | Asn | Lys | Pro | Asn | 145 | 150 | 155 | 160 |
| Asn | Asp | Phe | His | Phe | Glu | Val | Phe | Asn | Phe | Val | Pro | Cys | Ser | Ile | Cys | 165 | 170 | 175 | |
| Ser | Asn | Asn | Pro | Thr | Cys | Trp | Ala | Ile | Cys | Lys | Arg | Ile | Pro | Asn | Lys | 180 | 185 | 190 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Pro | Gly | Lys | Lys | Thr | Thr | Thr | Lys | Pro | Thr | Lys | Lys | Pro | Thr | Phe |
| | | 195 | | | | | | 200 | | | | | 205 | | |
| | | | | | | | | | | | | | | | |
| Lys | Thr | Thr | Lys | Lys | Asp | Leu | Lys | Pro | Gln | Thr | Thr | Lys | Pro | Lys | Glu |
| | | 210 | | | | 215 | | | | | | 220 | | | |
| | | | | | | | | | | | | | | | |
| Val | Pro | Thr | Thr | Lys | Pro | Thr | Glu | Glu | Pro | Thr | Ile | Asn | Thr | Thr | Lys |
| | | 225 | | | | 230 | | | | | 235 | | | | 240 |
| | | | | | | | | | | | | | | | |
| Thr | Asn | Ile | Thr | Thr | Thr | Leu | Leu | Thr | Asn | Asn | Thr | Thr | Gly | Asn | Pro |
| | | | | | | 245 | | | | 250 | | | | | 255 |
| | | | | | | | | | | | | | | | |
| Lys | Leu | Thr | Ser | Gln | Met | Glu | Thr | Phe | His | Ser | Thr | Ser | Ser | Glu | Gly |
| | | | | | | 260 | | | | 265 | | | | 270 | |
| | | | | | | | | | | | | | | | |
| Asn | Leu | Ser | Pro | Ser | Gln | Val | Ser | Thr | Thr | Ser | Glu | His | Pro | Ser | Gln |
| | | | | | | 275 | | | | 280 | | | 285 | | |
| | | | | | | | | | | | | | | | |
| Pro | Ser | Ser | Pro | Pro | Asn | Thr | Thr | Arg | Gln | | | | | | |
| | | | | | | 290 | | | 295 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATCAATCAAA GGCCTGTGA TAATAG

26

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGACTTGA TAATGAG

17

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | |
|---|----|
| AATTCATGGA GTTGCTAATC CTCAAAGCAA ATGCAATTAC CACAATCCTC ACTGCAGTCA | 60 |
| CATTTTGTTT TGCTTCTGGT TCTAAG | 86 |

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | |
|-------------------------------|----|
| ACTGGCATCA ATCTAGCACT ACATGAG | 27 |
|-------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | |
|---|-----|
| AATTCATGCC AACTTTAATA CTGCTAATTA TTACAACAAT GATTATGGCA TCTTCCTGCC | 60 |
| AAATAGATAT CACAAAATA CAGCATGTAG GTGTATTGGT CAACAGTCCC AAAGGGATGA | 120 |
| AGATATCACA AAACCTT | 136 |

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTTC 60
GTAACAGTTT TGTAATAAAA AAACCTATAA ATAG 94

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTTC 60
GTAACAGTTT TGTAATAAAA AAACCTATAA ATATTCCGGA ATTCAGATCT GCAGCGGCCG 120
CTCCATCTAG AAGGTACCCG G 141

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATGACTAAT TCCATCAAAA GTGAAAAGGC T 31

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAAGAAAAAG GAATAAAA 18

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATTTCTGTGA TATTTGTGCG GTATAATGAT GCTATACCT

39

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAGGAGAAGG GTATCAAG

18

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGGAGAAGGG TATCAAG

17

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCATGGAGA TAATTAAAAT GATAACCATC TCGCAAATAA ATAAGTATTT TACTGTTTTTC

60

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gln Glu Lys Gly Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gln Glu Lys Gly Ile Lys
1 5

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCAATCTAG CACTACACAG

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1617 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | |
|--|------|
| ATGCCAACTT TAATACTGCT AATTATTACA ACAATGATTA TGGCATCTTC CTGCCAAATA | 60 |
| GATATCACAA AACTACAGCA TGTAGGTGTA TTGGTCAACA GTCCCAAAGG GATGAAGATA | 120 |
| TCACAAAAC TCGAAACAAG ATATCTAATT TTGAGCCTCA TACCAAAAAT AGAAGACTCT | 180 |
| AACTCTTGTG GTGACCAACA GATCAAACAA TACAAGAGGT TATTGGATAG ACTGATCATC | 240 |
| CCTCTATATG ATGGATTAAG ATTACAGAAA GATGTGATAG TAACCAATCA AGAATCCAAT | 300 |
| GAAAACACTG ATCCCAGAAC AAGACGATCC TTTGGAGGGG TAATTGGAAC CATTGCTCTG | 360 |
| GGAGTAGCAA CCTCAGCACA AATTACAGCG GCAGTTGCTC TGGTTGAAGC CAAGCAGGCA | 420 |
| AAATCAGACA TCGAAAAACT CAAAGAAGCA ATCAGGGACA CAAACAAAGC AGTGCAGTCA | 480 |
| GTTTCAGAGCT CTATAGGAAA TTTAATAGTA GCAATTAAAT CAGTCCAAGA TTATGTCAAC | 540 |
| AACGAAATGG TGCCATCGAT TGCTAGACTA GGTGTGAAG CAGCAGGACT TCAATTAGGA | 600 |
| ATTGCATTAA CACAGCATT A CTCAGAATTA ACAAACATAT TTGGTGATAA CATAGGATCG | 660 |
| TTACAAGAAA AAGGAATAAA ATTACAAGGT ATAGCATCAT TATACCGCAC AAATATCACA | 720 |
| GAAATATTCA CAACATCAAC AGTTGATAAA TATGATATCT ATGATCTATT ATTTACAGAA | 780 |
| TCAATAAAGG TGAGAGTTAT AGATGTTGAT TTGAATGATT ACTCAATCAC CCTCCAAGTC | 840 |
| AGACTCCCTT TATTAAGTAG GCTGCTGAAC ACTCAGATCT ACAAAGTAGA TTCCATATCA | 900 |
| TATAATATCC AAAACAGAGA ATGGTATATC CCTCTTCCCA GCCATATCAT GACGAAAGGG | 960 |
| GCATTTCTAG GTGGAGCAGA TGTCAAGGAA TGTATAGAAG CATTTCAGCAG TTATATATGC | 1020 |
| CCTTCTGATC CAGGATTTGT ACTAAACCAT GAAATGGAGA GCTGCTTATC AGGAAACATA | 1080 |
| TCCCAATGTC CAAGAACCAC GGTCACATCA GACATTGTTT CAAGATATGC ATTTGTCAAT | 1140 |
| GGAGGAGTGG TTGCAAAC TATAACAACC ACCTGTACAT GCAACGGAAT CGACAATAGA | 1200 |
| ATCAATCAAC CACCTGATCA AGGAGTAAAA ATTATAACAC ATAAAGAATG TAATACAATA | 1260 |
| GGTATCAACG GAATGCTGTT CAATACAAAT AAAGAAGGAA CTCTTGCAAT CTACACACCA | 1320 |
| AATGATATAA CACTAAATAA TTCTGTTGCA CTTGATCCAA TTGACATATC AATCGAGCTT | 1380 |
| AACAAAGCCA AATCAGATCT AGAAGAATCA AAAGAATGGA TAAGAAGGTC AAATCAAAAA | 1440 |
| CTAGATTCTA TTGGAAACTG GCATCAATCT AGCACTACAA TCATAATTAT TTTAATAATG | 1500 |
| ATCATTATAT TGTTTATAAT TAATGTAACG ATAATTACAA TTGCAATTAA GTATTACAGA | 1560 |
| ATTCAAAAGA GAAATCGAGT GGATCAAAAT GACAAGCCAT ATGTACTAAC AAACAAA | 1617 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1715 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | |
|--|------|
| ATGGAATACT GGAAGCATAC CAATCACGGA AAGGATGCTG GCAATGAGCT GGAGACGTCC | 60 |
| ATGGCTACTA ATGGCAACAA GCTCACCAAT AAGATAACAT ATATATTATG GACAATAATC | 120 |
| CTGGTGTTAT TATCAATAGT CTTCATCATA GTGCTAATTA ATTCCATCAA AAGTGAAAAG | 180 |
| GCTCATGAAT CATTGCTGCA AGACATAAAT AATGAGTTTA TGGAAATTAC AGAAAAGATC | 240 |
| CAAATGGCAT CGGATAATAC CAATGATCTA ATACAGTCAG GAGTGAATAC AAGGCTTCTT | 300 |
| ACAATTCAGA GTCATGTCCA GAATTATATA CCAATATCAC TGACACAACA GATGTCAGAT | 360 |
| CTTAGGAAAT TCATTAGTGA AATTACAATT AGAAATGATA ATCAAGAAGT GCTGCCACAA | 420 |
| AGAATAACAC ATGATGTGGG TATAAAACCT TTAAATCCAG ATGATTTTTG GAGATGCACG | 480 |
| TCTGGTCTTC CATCTTTAAT GAAAACTCCA AAAATAAGGT TAATGCCAGG GCCGGGATTA | 540 |
| TTAGCTATGC CAACGACTGT TGATGGCTGT ATCAGAACTC CGTCCTTAGT TATAAATGAT | 600 |
| CTGATTTATG CTTATACCTC AAATCTAATT ACTCGAGGTT GTCAGGATAT AGGAAAATCA | 660 |
| TATCAAGTCT TACAGATAGG GATAATAACT GTAACTCAG ACTTGGTACC TGACTTAAAT | 720 |
| CCCAGGATCT CTCATACTTT TAACATAAAT GACAATAGGA AGTCATGTTT TCTAGCACTC | 780 |
| CTAAATACAG ATGTATATCA ACTGTGTTCA ACTCCCAAAG TTGATGAAAG ATCAGATTAT | 840 |
| GCATCATCAG GCATAGAAGA TATTGTACTT GATATTGTCA ATTATGATGG CTCAATCTCA | 900 |
| ACAACAAGAT TTAAGAATAA TAACATAAGC TTTGATCAAC CTTATGCTGC ACTATACCCA | 960 |
| TCTGTTGGAC CAGGGATATA CTACAAAGGC AAAATAATAT TTCTCGGGTA TGGAGGTCTT | 1020 |
| GAACATCCAA TAAATGAGAA TGTAATCTGC AACACAACCT GGTGTCCCGG GAAAACACAG | 1080 |
| AGAGACTGCA ATCAGGCATC TCATAGTCCA TGGTTTTTCAG ATAGGAGGAT GGTCAACTCT | 1140 |
| ATCATTGTTG TTGACAAAGG CTTAACTCA ATTCCAAAAT TGAAGGTATG GACGATATCT | 1200 |
| ATGAGACAGA ATTACTGGGG GTCAGAAGGA AGGTTACTTC TACTAGGTAA CAAGATCTAT | 1260 |
| ATATATACAA GATCCACAAG TTGGCATAGC AAGTTACAAT TAGGAATAAT TGATATTACT | 1320 |
| GATTACAGTG ATATAAGGAT AAAATGGACA TGGCATAATG TGCTATCAAG ACCAGGAAAC | 1380 |

| | |
|---|------|
| AATGAATGTC CATGGGGACA TTCATGTCCA GATGGATGTA TAACAGGAGT ATATACTGAT | 1440 |
| GCATATCCAC TCAATCCCAC AGGGAGCATT GTGTCATCTG TCATATTAGA TTCACAAAAA | 1500 |
| TCGAGAGTGA ACCCAGTCAT AACTTACTCA ACAGCAACCG AAAGAGTAAA CGAGCTGGCC | 1560 |
| ATCCGAAACA GAACACTCTC AGCTGGATAT ACAACAACAA GCTGCATCAC ACACTATAAC | 1620 |
| AAAGGATATT GTTTTCATAT AGTAGAAATA AATCAGAAAA GCTTAAACAC ACTTCAACCC | 1680 |
| ATGTTGTTCA AGACAGAGGT TCCAAAAAGC TGCAG | 1715 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | |
|---|-----|
| ATGGAGTTGC CAATCCTCAA AGCAAATGCA ATTACCACAA TCCTCGCTGC AGTCACATTT | 60 |
| TGCTTTGCTT CTAGTCAAAA CATCACTGAA GAATTTTATC AATCAACATG CAGTGCAGTT | 120 |
| AGCAAAGGCT ATCTTAGTGC TCTAAGAACT GGTGGGTATA CTAGTGTTAT AACTATAGAA | 180 |
| TTAAGTAATA TCAAGGAAAA TAAGTGTAAT GGAACAGATG CTAAGGTAAA ATTGATGAAA | 240 |
| CAAGAATTAG ATAAATATAA AAATGCTGTA ACAGAATTGC AGTTGCTCAT GCAAAGCACA | 300 |
| CCAGCAGCAA ACAATCGAGC CAGAAGAGAA CTACCAAGGT TTATGAATTA TACACTCAAC | 360 |
| AATACCAAAA AAACCAATGT AACATTAAGC AAGAAAAGGA AAAGAAGATT TCTTGGTTTT | 420 |
| TTGTTAGGTG TTGGATCTGC AATCGCCAGT GGCATTGCTG TATCTAAGGT CCTGCACTTA | 480 |
| GAAGGAGAAG TGAACAAGAT CAAAAGTGCT CTACTATCCA CAAACAAGGC CGTAGTCAGC | 540 |
| TTATCAAATG GAGTTAGTGT CTTAACCAGC AAAGTGTTAG ACCTCAAAAA CTATATAGAT | 600 |
| AAACAATTGT TACCTATTGT GAATAAGCAA AGCTGCAGAA TATCAAATAT AGAACTGTG | 660 |
| ATAGAGTTCC AACAAAAGAA CAACAGACTA CTAGAGATTA CCAGGGAATT TAGTGTTAAT | 720 |
| GCAGGTGTAA CTACACCTGT AAGCACTTAC ATGTTAACTA ATAGTGAATT ATTGTCATTA | 780 |
| ATCAATGATA TGCCTATAAC AAATGATCAG AAAAAGTTAA TGTCCAACAA TGTTCAAATA | 840 |
| GTTAGACAGC AAAGTTACTC TATCATGTCC ATAATAAAAG AGGAAGTCTT AGCATATGTA | 900 |
| GTACAATTAC CACTATATGG TGTGATAGAT ACACCTTGTT GGAAATTACA CACATCCCCT | 960 |

| | |
|--|------|
| CTATGTACAA CCAACACAAA AGAAGGGTCA AACATCTGTT TAACAAGAAC TGACAGAGGA | 1020 |
| TGGTACTGTG ACAATGCAGG ATCAGTATCT TTCTTCCCAC AAGCTGAAAC ATGTAAAGTT | 1080 |
| CAATCGAATC GAGTATTTTG TGACACAATG AACAGTTTAA CATTACCAAG TGAAGTAAAT | 1140 |
| CTCTGCAATG TTGACATATT CAATCCCAAA TATGATTGTA AAATTATGAC TTCAAAAACA | 1200 |
| GATGTAAGCA GCTCCGTTAT CACATCTCTA GGAGCCATTG TGTCATGCTA TGGCAAAACT | 1260 |
| AAATGTACAG CATCCAATAA AAATCGTGGA ATCATAAAGA CATTTTCTAA CGGGTGTGAT | 1320 |
| TATGTATCAA ATAAAGGGGT GGACACTGTG TCTGTAGGTA ACACATTATA TTATGTAAAT | 1380 |
| AAGCAAGAAG GCAAAAGTCT CTATGTAAAA GGTGAACCAA TAATAAATTT CTATGACCCA | 1440 |
| TTAGTATTCC CCTCTGATGA ATTTGATGCA TCAATATCTC AAGTCAATGA GAAGATTAAC | 1500 |
| CAGAGTTTAG CATTTATTCTG TAAATCCGAT GAATTATTAC ATAATGTAAA TGCTGGTAAA | 1560 |
| TCAACCACAA ATATCATGAT AACTACTATA ATTATAGTGA TTATAGTAAT ATTGTTATCA | 1620 |
| TTAATTGCTG TTGGACTGCT CCTATACTGT AAGGCCAGAA GCACACCAGT CACACTAAGC | 1680 |
| AAGGATCAAC TGAGTGGTAT AAATAATATT GCATTTAGTA AC | 1722 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | |
|--|-----|
| ATGTCCAAAA ACAAGGACCA ACGCACCGCT AAGACACTAG AAAAGACCTG GGACACTCTC | 60 |
| AATCATTTAT TATTCATATC ATCGGGCTTA TATAAGTTAA ATCTTAAATC TGTAGCACAA | 120 |
| ATCACATTAT CCATTCTGGC AATGATAATC TCAACTTCAC TTATAATTAC AGCCATCATA | 180 |
| TTCATAGCCT CGGCAAACCA CAAAGTCACA CTAACAACCTG CAATCATACA AGATGCAACA | 240 |
| AGCCAGATCA AGAACACAAC CCCAACATAC CTCACTCAGG ATCCTCAGCT TGGAATCAGC | 300 |
| TTCTCCAATC TGTCTGAAAT TACATCACAA ACCACCACCA TACTAGCTTC AACAACACCA | 360 |
| GGAGTCAAGT CAAACCTGCA ACCCACAACA GTCAAGACTA AAAACACAAC AACCAACCCAA | 420 |
| ACACAACCCA GCAAGCCCAC TACAAAACAA CGCCAAAACA AACCACCAA CAAACCCAAT | 480 |
| AATGATTTTC ACTTCGAAGT GTTTAACTTT GTACCCTGCA GCATATGCAG CAACAATCCA | 540 |

| | |
|---|-----|
| ACCTGCTGGG CTATCTGCAA AAGAATACCA AACAAAAAAC CAGGAAAGAA AACCACCACC | 600 |
| AAGCCTACAA AAAAACCAAC CTTCAAGACA ACCAAAAAG ATCTCAAACC TCAAACCACT | 660 |
| AAACCAAAGG AAGTACCCAC CACCAAGCCC ACAGAAGAGC CAACCATCAA CACCACCAA | 720 |
| ACAAACATCA CAACTACACT GCTCACCAAC AACACCACAG GAAATCCAAA ACTCACAAGT | 780 |
| CAAATGGAAA CCTTCCACTC AACCTCCTCC GAAGGCAATC TAAGCCCTTC TCAAGTCTCC | 840 |
| ACAACATCCG AGCACCCATC ACAACCCTCA TCTCCACCCA ACACAACACG CCAG | 894 |

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | |
|-------------------------------------|----|
| CGTAGTTAGT TTCCAGGACA CTATTATCCT AG | 32 |
|-------------------------------------|----|

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | |
|--------------------|----|
| TGAACTATTA CTCCTAG | 17 |
|--------------------|----|

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | |
|--|----|
| GTACCTCAAC GATTAGGAGT TTCGTTTACG TTAATGGTGT TAGGAGTGAC GTCAGTGTA | 60 |
|--|----|

AACAAAACGA AGACCAAGAT TCCAG

85

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGTAGTTAGA TCGTGATGTA CTCCTAG

27

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTACGGTTGA AATTATGACG ATTAATAATG TTGTTACTAA TACCGTAGAA GGACGGTTTA
TCTATAGTGT TTTGATGTCG TACATCCACA TAACCAGTTG TCAGGGTTTC CCTACTTCTA
TAGTGTTTTG AAGCTT

60

120

136

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TAGTACCTCT ATTAATTTTA CTATTGGTAG AGCGTTTATT TATTCATAAA ATGACAAAAG
CATTGTCAAA ACATTATTTT TTTGGATATT TATCTTAA

60

98

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
TAGTACCTCT ATTAATTTTA CTATTGGTAG AGCGTTTATT TATTCATAAA ATGACAAAAG      60
CATTGTCAAA ACATTATTTT TTTGGATATT TATAAGGCCT TAAGTCTAGA CGTCGCCGGC      120
GAGGTAGATC TTCCATGGGC CCTAG                                           145
```

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
TGATTAAGGT AGTTTTCACT TTTCCGAGTA C                                     31
```

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
TAAAGACACT ATAAACACGC CATATTACTA CGATATGGA                             39
```

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGGACAAAAG

10